

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:14:14 ; Search time 7 Seconds
(without alignments)
282.548 Million cell updates/sec

Title: US-10-057-890A-8
Perfect score: 40
Sequence: 1 TGEKPYK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	40	100.0	7	5	ABG32537	Abg32537 Human Kru
2	40	100.0	14	4	AAM00144	Aam00144 Human tra
3	40	100.0	15	4	AAB47434	Aab47434 Human zin
4	40	100.0	28	5	AAM47783	Aam47783 Human myo
5	40	100.0	34	4	AAU08504	Aau08504 Zinc fing
6	40	100.0	43	4	ABG01497	Abg01497 Novel hum
7	40	100.0	73	5	ABP64639	Abp64639 Human ORF
8	40	100.0	77	4	AAO05583	Aao05583 Human pol
9	40	100.0	84	3	AAY88345	Aay88345 Synthetic

10	40	100.0	84	3	AAy88344	Aay88344	Synthetic
11	40	100.0	84	5	AAE21142	Aae21142	Zinc fing
12	40	100.0	84	5	AAE21146	Aae21146	Mutant zi
13	40	100.0	84	5	AAE21145	Aae21145	Mutant zi
14	40	100.0	84	7	AAE38681	Aae38681	Zinc fing
15	40	100.0	88	5	ABP01014	Abp01014	Human ORF
16	40	100.0	89	4	AAO08151	Aao08151	Human pol
17	40	100.0	90	5	ABP48203	Abp48203	Sp-1 zinc
18	40	100.0	90	6	AAE36755	Aae36755	Zinc fing
19	40	100.0	90	6	ABP70153	Abp70153	Amino aci
20	40	100.0	90	7	ADA62044	Ada62044	Zinc fing
21	40	100.0	91	6	ABR41417	Abr41417	Human DIT
22	40	100.0	91	7	ADE31131	Ade31131	Human dia
23	40	100.0	97	5	ABG60032	Abg60032	Human DIT
24	40	100.0	99	5	AAE21127	Aae21127	Zinc fing
25	40	100.0	99	5	AAE21125	Aae21125	Zinc fing
26	40	100.0	99	5	AAE21129	Aae21129	Zinc fing
27	40	100.0	99	5	AAE21130	Aae21130	Zinc fing
28	40	100.0	99	5	AAE21126	Aae21126	Zinc fing
29	40	100.0	99	5	AAE21128	Aae21128	Zinc fing
30	40	100.0	99	6	ABO01250	Abo01250	Zinc fing
31	40	100.0	99	7	AAE38665	Aae38665	Zinc fing
32	40	100.0	99	7	AAE38666	Aae38666	Zinc fing
33	40	100.0	99	7	AAE38667	Aae38667	Zinc fing
34	40	100.0	99	7	AAE38664	Aae38664	Zinc fing
35	40	100.0	99	7	AAE38668	Aae38668	Zinc fing
36	40	100.0	99	7	AAE38669	Aae38669	Zinc fing
37	40	100.0	100	3	AAB14294	Aab14294	Transcrip
38	40	100.0	100	5	ABG59960	Abg59960	Human DIT
39	40	100.0	100	5	ABJ03954	Abj03954	Zinc fing
40	40	100.0	100	6	AAE30447	Aae30447	Spl trans
41	40	100.0	100	6	ABO14614	Abo14614	Zinc fing
42	40	100.0	104	4	AAU16429	Aau16429	Human nov
43	40	100.0	104	4	AAU16371	Aau16371	Human nov
44	40	100.0	104	4	AAU20295	Aau20295	Human nov
45	40	100.0	104	6	ABU55440	Abu55440	Human nov

ALIGNMENTS

RESULT 1

ABG32537

ID ABG32537 standard; peptide; 7 AA.

XX

AC ABG32537;

XX

DT 15-NOV-2002 (first entry)

XX

DE Human Kruppel-type linker peptide.

XX

KW Scaffolded protein; CCR5; HIV; human immunodeficiency virus infection;

KW ECD; extracellular domain; metal chelating motif; zinc finger protein;

KW integral membrane protein; soluble loop; intracellular domain; ICD;

KW gene therapy; immunogen; viral infection; human;

KW Kruppel-type linker peptide.

XX

OS Homo sapiens.
 XX
 PN WO200260477-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 29-JAN-2002; 2002WO-US002377.
 XX
 PR 31-JAN-2001; 2001US-0265782P.
 PR 31-JAN-2001; 2001US-0265858P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Coleman TA, Mansfield B;
 XX
 DR WPI; 2002-643357/69.
 XX
 PT Novel scaffolded fusion polypeptide useful for therapeutic purposes or
 PT for screening molecules that bind/activate/inhibit/modulate the
 PT polypeptide, comprises a functional polypeptide domain fused to a
 PT scaffold domain.
 XX
 PS Disclosure; Page 19; 64pp; English.
 XX
 CC The invention relates to a scaffolded fusion polypeptide comprising a
 CC functional polypeptide domain fused to a scaffold domain, where the
 CC functional polypeptide domain corresponds to a soluble loop of an
 CC integral membrane protein (e.g. human CCR5, a transmembrane receptor
 CC involved in HIV (human immunodeficiency virus) infection). Also included
 CC are; (1) a polypeptide comprising a scaffold domain; (2) a nucleic acid
 CC encoding the fusion polypeptide; (3) a vector cassette for the expression
 CC of the fusion polypeptide comprising an expression region operably linked
 CC to a promoter, where the expression region comprises a number of
 CC cassettes, each of which encodes a module, domain or strand of the fusion
 CC polypeptide and (4) a host cell comprising the vector or nucleic acid.
 CC The fusion polypeptide is useful for screening molecules that
 CC bind/activate/inhibit/modulate the fusion polypeptide, by expressing the
 CC fusion polypeptide from and identifying a molecule that binds to the
 CC fusion polypeptide. The fusion polypeptide is useful in diagnostic
 CC methods, in assays to identify compounds that interact with loops of
 CC fragments of an extracellular domain (ECD) or an intracellular domain
 CC (ICD) or to rapidly assay the function of mutated portions of mutant
 CC integral membrane proteins without having to produce significant
 CC quantities of the entire mutant integral membrane protein, to generate
 CC antibodies that recognise the integral membrane proteins from which they
 CC are designed, to competitively bind the ligand of a naturally occurring
 CC receptor in vitro or in vivo, to display and/or screen soluble domains
 CC from protein such as integral membrane proteins, to probe the structure
 CC of ECD or ICD, or both, of an integral protein membrane, to modulate the
 CC activity of a receptor in vivo, and for treating or preventing viral
 CC infection, preferably human HIV infection e.g. by gene therapy using the
 CC encoding nucleic acid. The present sequence is a Kruppel-type linker
 CC peptide suitable for inclusion in the fusion protein of the invention
 XX
 SQ Sequence 7 AA;

Query Match

100.0%; Score 40; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
Db 1 TGEKPYK 7

RESULT 2

AAM00144

ID AAM00144 standard; peptide; 14 AA.

XX

AC AAM00144;

XX

DT 01-OCT-2001 (first entry)

XX

DE Human transcription factor fragment SEQ ID NO: 684.

XX

KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.

XX

OS Homo sapiens.

XX

PN WO200151670-A2.

XX

PD 19-JUL-2001.

XX

PF 05-JAN-2001; 2001WO-US000322.

XX

PR 07-JAN-2000; 2000US-0174962P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach MD;

XX

DR WPI; 2001-451871/48.

DR N-PSDB; AAH89253.

XX

PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.

XX

PS Disclosure; Page 301; 475pp; English.

XX

CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberos
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a pepttide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention

XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 40; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 1 TGEKPYK 7

RESULT 3

AAB47434

ID AAB47434 standard; peptide; 15 AA.

XX

AC AAB47434;

XX

DT 31-OCT-2001 (first entry)

XX

DE Human zinc-finger protein 43 N-terminal fragment.

XX

KW Human; zinc-finger protein 43; TFIIS; diagnosis; malignant tumor;
KW hemopathy; HIV; inflammation.

XX

OS Homo sapiens.

XX

PN WO200155426-A1.

XX

PD 02-AUG-2001.

XX

PF 15-JAN-2001; 2001WO-CN000056.

XX

PR 26-JAN-2000; 2000CN-00111527.

XX

PA (BIOD-) BIODOR GENE TECHNOLOGY LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2001-483266/52.

XX

PT Human zinc-finger protein 43 containing TFIIS characteristic sequence
PT fragment and encoded polynucleotide, applicable in diagnosis and
PT treatment of malignant tumor, hemopathy, HIV infection, immunological
PT diseases and various inflammations.

XX

PS Example 6; Page 42; 46pp; Chinese.

XX

CC This sequence represents the N-terminal fragment of human zinc-finger
CC protein 43. The human zinc-finger protein 43 contains a TFIIS
CC characteristic sequence. The polypeptide and encoded polynucleotide may
CC be used in diagnosis and treatment of malignant tumor, hemopathy, HIV
CC infection, immunological diseases and various inflammations

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 40; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
Db 3 TGEKPYK 9

RESULT 4

AAM47783

ID AAM47783 standard; peptide; 28 AA.

XX

AC AAM47783;

XX

DT 01-MAR-2002 (first entry)

XX

DE Human myoneurine fragment comprising C2H2 motif #2.

XX

KW Human; myoneurine; cytostatic; neurological; muscular; gene therapy;

KW cancer; neuromuscular disease; dystrophy; polymyositis; rhabdomyosarcoma;

KW C2H2.

XX

OS Homo sapiens.

XX

PN FR2808535-A1.

XX

PD 09-NOV-2001.

XX

PF 05-MAY-2000; 2000FR-00005792.

XX

PR 05-MAY-2000; 2000FR-00005792.

XX

PA (ALLI/) ALLIEL P M.

XX

PI Seddiqi N, Cifuentes DC, Rieger F, Perin JP;

XX

DR WPI; 2002-019508/03.

XX

PT New nucleic acid encoding human myoneurin, useful for diagnosis,
PT prognosis and treatment of cancer and neurological diseases, comprises a
PT polynucleotide encoding the human myoneurin protein.

XX

PS Claim 13; Page 59; 64pp; French.

XX

CC The present invention relates to human myoneurin (ABA04825 and AAM47779).

CC The myoneurin coding sequence and its fragments are useful as primers and

CC probes, for diagnosis, prognosis or assessing risk of human diseases,

CC particularly cancers and neuromuscular diseases (e.g. dystrophy,

CC polymyositis or rhabdomyosarcoma). The coding sequence and its fragments

CC are also useful in gene therapy for these diseases. The present sequence

CC is a fragment of the human myoneurin protein. This sequence comprises a

CC C2H2 motif

XX

SQ Sequence 28 AA;

Query Match 100.0%; Score 40; DB 5; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
Db 22 TGEKPYK 28

RESULT 5

AAU08504

ID AAU08504 standard; protein; 34 AA.

XX

AC AAU08504;

XX

DT 17-DEC-2001 (first entry)

XX

DE Zinc finger domain TG-ZFD-002.

XX

KW Zinc finger domain; cancer; human.

XX

OS Homo sapiens.

XX

PN WO200160970-A2.

XX

PD 23-AUG-2001.

XX

PF 17-FEB-2001; 2001WO-KR000244.

XX

PR 18-FEB-2000; 2000KR-00007730.

XX

PA (TOOL-) TOOLGEN INC.

XX

PI Kim J, Kwon Y, Kim H, Ryu EH, Hwang MS;

XX

DR WPI; 2001-557644/62.

DR N-PSDB; AAS13021.

XX

PT Identifying a zinc finger domain for e.g. designing new polypeptides that
PT bind to a specific site on a DNA, comprises expressing hybrid nucleic
PT acids with a test zinc finger domain in cells.

XX

PS Example 12; Page 50; 147pp; English.

XX

CC The invention relates to a method of identifying a zinc finger domain
CC that recognises a target site on a DNA. The method comprises expressing
CC hybrid nucleic acids with a test zinc finger domain in cells containing a
CC reporter construct, where the reporter gene is expressed above a given
CC level when a transcription factor recognises a recruitment and a target
CC site of a promoter, and not only the recruitment site of the promoter.
CC The method is used to: (a) identify a zinc finger domain that recognises
CC a target site on a DNA; (b) determine whether a test zinc finger domain
CC recognises a target site on a promoter; (c) generate a nucleic acid that
CC encodes a chimeric zinc finger protein; and (d) identify DNA sequences
CC recognised by zinc finger domains. The method can be used to design novel
CC polypeptides that bind to a specific site on a DNA. The method can
CC facilitate the customised generation of new polypeptides that can
CC regulate the expression a selected target e.g. a gene required by a
CC pathogen can be repressed, a gene required for cancerous growth can be
CC repressed, or a gene poorly expressed or encoding a mutated protein can
CC be activated and overexpressed. The method can be used in vivo which

CC enables identification of polypeptides that bind to a specific site on a
CC DNA in the intracellular milieu. The present sequence represents the
CC amino acid sequence of TG_ZFD-002 zinc finger protein which was used in
CC the method of the invention
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 40; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 1 TGEKPYK 7

RESULT 6

ABG01497

ID ABG01497 standard; protein; 43 AA.

XX

AC ABG01497;

XX

DT 13-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #1488.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR N-PSDB; AAS65684.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

PS Claim 20; SEQ ID NO 31856; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 43 AA;

Query Match 100.0%; Score 40; DB 4; Length 43;
 Best Local Similarity 100.0%; Pred. No. 0.95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 35 TGEKPYK 41

RESULT 7

ABP64639

ID ABP64639 standard; protein; 73 AA.

XX

AC ABP64639;

XX

DT 04-NOV-2002 (first entry)

XX

DE Human ORF1009.

XX

KW Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary;
 KW Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet;
 KW human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;
 KW cancer; cardiovascular disease; allergy; autoimmune disease;
 KW wound healing; blood coagulation disorder; inflammatory disorder.

XX

OS Homo sapiens.

XX

PN US2002082206-A1.

XX

PD 27-JUN-2002.

XX

PF 30-MAY-2001; 2001US-00867550.

XX

PR 30-MAY-2000; 2000US-0208427P.

XX

PA (LEAC/) LEACH M D.

PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.

XX

PI Leach MD, Mehraban F, Conley PB, Topper JN, Law D;

XX

DR WPI; 2002-626554/67.

DR N-PSDB; ABQ99202.

XX

PT New polypeptide designated ORFX are present in human atherogenic cells
PT and are useful to prevent and treat ORFX-associated disorders including
PT cancer, allergy, wound healing or autoimmune, cardiovascular or
PT inflammatory disease.

XX

PS Claim 10; SEQ ID NO 2018; 78pp; English.

XX

CC The present invention relates to novel human ORFX polypeptides and their
CC coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences
CC were discovered in human atherogenic cells, in particular in platelets
CC and human umbilical vein endothelial cells (HUVEC) and are expressed in
CC many other tissues as well. Atherogenic cells are cells which have the
CC potential to develop atherosclerotic plaques. The ORFX polypeptides and
CC nucleic acids are useful for treating or preventing a pathological
CC condition associated with an ORFX-associated disorder, e.g. cancer,
CC cardiovascular disease, allergy, autoimmune disease, wound healing, blood
CC coagulation disorders or inflammatory disorders. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/sequence.html?DocID=20020082206

XX

SQ Sequence 73 AA;

Query Match 100.0%; Score 40; DB 5; Length 73;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGEKPYK 7

|||||||

Db 17 TGEKPYK 23

RESULT 8

AAO05583

ID AAO05583 standard; protein; 77 AA.

XX

AC AAO05583;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 19475.

XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorders; arthritis; inflammation.

XX

OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US004927.
 XX
 PR 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AAI85514.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 PS Claim 20; SEQ ID NO 19475; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 77 AA;

Query Match 100.0%; Score 40; DB 4; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGEKPYK 7
 |||||
 Db 17 TGEKPYK 23

RESULT 9
 AAY88345
 ID AAY88345 standard; protein; 84 AA.
 XX
 AC AAY88345;
 XX
 DT 14-JUL-2000 (first entry)
 XX
 DE Synthetic protein consisting of three zinc finger domains.

XX
 KW Zinc finger repeat sequence; gene library; specific binding interaction;
 KW protein identification method; selection; screening.
 XX
 OS Synthetic.
 XX
 PN WO200015777-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 14-SEP-1999; 99WO-GB003081.
 XX
 PR 14-SEP-1998; 98EP-00307434.
 XX
 PA (UYAS-) UNIV ASTON.
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH UK LTD.
 XX
 PI Hine AV, Morgan LJ, Santos AF, Palfrey D;
 XX
 DR WPI; 2000-271418/23.
 XX
 PT Set of libraries of genes which code for proteins capable of specific
 PT binding interactions are used as selection or screening strategies in a
 PT combinatorial approach to obtain novel proteins capable of binding a
 PT desired target molecule.
 XX
 PS Example; Page 32; 48pp; English.
 XX
 CC This sequence represents a synthetic protein which contains three
 CC consensus zinc finger repeat sequences. The invention relates to a set of
 CC libraries of genes which code for proteins which are capable of specific
 CC binding interactions using amino acid residues at two or more determined
 CC positions. The present sequence represents a protein encoded by the genes
 CC in the libraries of the invention. The libraries of the invention can be
 CC used in a method of identifying a protein which interacts with a specific
 CC binding partner. The libraries and methods are useful as selection or
 CC screening strategies in a combinatorial approach to obtain novel proteins
 CC capable of binding a desired target molecule
 XX
 SQ Sequence 84 AA;

Query Match 100.0%; Score 40; DB 3; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 1 TGEKPYK 7

RESULT 10
 AAY88344
 ID AAY88344 standard; protein; 84 AA.
 XX
 AC AAY88344;
 XX
 DT 14-JUL-2000 (first entry)

XX
DE Synthetic protein consisting of three zinc finger domains.
XX
KW Zinc finger repeat sequence; gene library; specific binding interaction;
KW protein identification method; selection; screening.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 17
FT /note= "Any amino acid"
FT Misc-difference 20
FT /note= "Any amino acid"
FT Misc-difference 23
FT /note= "Any amino acid"
FT Misc-difference 45
FT /note= "Any amino acid"
FT Misc-difference 48
FT /note= "Any amino acid"
FT Misc-difference 51
FT /note= "Any amino acid"
FT Misc-difference 73
FT /note= "Any amino acid"
FT Misc-difference 76
FT /note= "Any amino acid"
FT Misc-difference 79
FT /note= "Any amino acid"
XX
PN WO200015777-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GB003081.
XX
PR 14-SEP-1998; 98EP-00307434.
XX
PA (UYAS-) UNIV ASTON.
PA (AMSH) AMERSHAM PHARMACIA BIOTECH UK LTD.
XX
PI Hine AV, Morgan LJ, Santos AF, Palfrey D;
XX
DR WPI; 2000-271418/23.
XX
PT Set of libraries of genes which code for proteins capable of specific
PT binding interactions are used as selection or screening strategies in a
PT combinatorial approach to obtain novel proteins capable of binding a
PT desired target molecule.
XX
PS Claim 6; Page 37; 48pp; English.
XX
CC This sequence represents a synthetic protein which contains three
CC consensus zinc finger repeat sequences. The invention relates to a set of
CC libraries of genes which code for proteins which are capable of specific
CC binding interactions using amino acid residues at two or more determined
CC positions. The present sequence represents a protein encoded by the genes
CC in the libraries of the invention. The libraries of the invention can be
CC used in a method of identifying a protein which interacts with a specific

CC binding partner. The libraries and methods are useful as selection or
CC screening strategies in a combinatorial approach to obtain novel proteins
CC capable of binding a desired target molecule
XX
SQ Sequence 84 AA;

Query Match 100.0%; Score 40; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 1 TGEKPYK 7

RESULT 11

AAE21142

ID AAE21142 standard; protein; 84 AA.

XX

AC AAE21142;

XX

DT 01-JUL-2002 (first entry)

XX

DE Zinc finger protein containing three zinc finger domains.

XX

KW DNA binding protein; zinc finger domain; zinc finger protein; ZFP;

KW viral replication; gene expression; virucide.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 15

FT /label= Asp, Gly

XX

PN WO200208286-A2.

XX

PD 31-JAN-2002.

XX

PF 19-JUL-2001; 2001WO-EP008367.

XX

PR 21-JUL-2000; 2000US-0220060P.

XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX

PI Sera T;

XX

DR WPI; 2002-172000/22.

XX

PT New Zinc Finger Protein (ZFP) comprising three essential domains useful
PT for diagnosing diseases associated with abnormal genomic structure.

XX

PS Example 4; Page 68; 143pp; English.

XX

CC The present invention relates to novel DNA binding proteins comprising
CC zinc finger domains in which two histidine and two cysteine residues
CC coordinate a central zinc ion. The invention particularly relates to the
CC identification of a context-independent recognition code to design zinc

CC finger domains. The invention also relates to zinc finger proteins (ZFP)
CC designed using this recognition code. The ZFPs are useful for altering
CC genomic structure, inhibiting viral replication (where viral replication
CC is inhibited for plant virus, an animal virus or a human virus),
CC modulating gene expression, detecting an altered zinc finger recognition
CC sequence and diagnosing disease associated with abnormal genomic
CC structure. The present sequence is ZFP containing three zinc finger
CC domains

XX

SQ Sequence 84 AA;

Query Match 100.0%; Score 40; DB 5; Length 84;

Best Local Similarity 100.0%; Pred. No. 2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7

||||||

Db 25 TGEKPYK 31

RESULT 12

AAE21146

ID AAE21146 standard; protein; 84 AA.

XX

AC AAE21146;

XX

DT 01-JUL-2002 (first entry)

XX

DE Mutant zinc finger protein (X15G) containing three zinc finger domains.

XX

KW DNA binding protein; zinc finger domain; zinc finger protein; ZFP;

KW viral replication; gene expression; virucide; mutant; mutein.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 15

FT /note= "Wild type Xaa substituted with Gly"

XX

PN WO200208286-A2.

XX

PD 31-JAN-2002.

XX

PF 19-JUL-2001; 2001WO-EP008367.

XX

PR 21-JUL-2000; 2000US-0220060P.

XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX

PI Sera T;

XX

DR WPI; 2002-172000/22.

XX

PT New Zinc Finger Protein (ZFP) comprising three essential domains useful
PT for diagnosing diseases associated with abnormal genomic structure.

XX

PS Example 4; Page; 143pp; English.

XX
 CC The present invention relates to novel DNA binding proteins comprising
 CC zinc finger domains in which two histidine and two cysteine residues
 CC coordinate a central zinc ion. The invention particularly relates to the
 CC identification of a context-independent recognition code to design zinc
 CC finger domains. The invention also relates to zinc finger proteins (ZFP)
 CC designed using this recognition code. The ZFPs are useful for altering
 CC genomic structure, inhibiting viral replication (where viral replication
 CC is inhibited for plant virus, an animal virus or a human virus),
 CC modulating gene expression, detecting an altered zinc finger recognition
 CC sequence and diagnosing disease associated with abnormal genomic
 CC structure. The present sequence is mutant ZFP (X15G) containing three
 CC zinc finger domains. Note: This sequence is not shown in the
 CC specification but is derived from wild type ZFP protein shown as SEQ ID
 CC NO: 30 in page 68 of the specification (AAE21142)
 XX
 SQ Sequence 84 AA;

Query Match 100.0%; Score 40; DB 5; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 25 TGEKPYK 31

RESULT 13

AAE21145

ID AAE21145 standard; protein; 84 AA.

XX

AC AAE21145;

XX

DT 01-JUL-2002 (first entry)

XX

DE Mutant zinc finger protein (X15D) containing three zinc finger domains.

XX

KW DNA binding protein; zinc finger domain; zinc finger protein; ZFP;

KW viral replication; gene expression; virucide; mutant; mutein.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 15

FT /note= "Wild type Xaa substituted with Asp"

XX

PN WO200208286-A2.

XX

PD 31-JAN-2002.

XX

PF 19-JUL-2001; 2001WO-EP008367.

XX

PR 21-JUL-2000; 2000US-0220060P.

XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX

PI Sera T;

XX
 DR WPI; 2002-172000/22.
 XX
 PT New Zinc Finger Protein (ZFP) comprising three essential domains useful
 PT for diagnosing diseases associated with abnormal genomic structure.
 XX
 PS Example 4; Page; 143pp; English.
 XX
 CC The present invention relates to novel DNA binding proteins comprising
 CC zinc finger domains in which two histidine and two cysteine residues
 CC coordinate a central zinc ion. The invention particularly relates to the
 CC identification of a context-independent recognition code to design zinc
 CC finger domains. The invention also relates to zinc finger proteins (ZFP)
 CC designed using this recognition code. The ZFPs are useful for altering
 CC genomic structure, inhibiting viral replication (where viral replication
 CC is inhibited for plant virus, an animal virus or a human virus),
 CC modulating gene expression, detecting an altered zinc finger recognition
 CC sequence and diagnosing disease associated with abnormal genomic
 CC structure. The present sequence is mutant ZFP (X15D) containing three
 CC zinc finger domains. Note: This sequence is not shown in the
 CC specification but is derived from wild type ZFP protein shown as SEQ ID
 CC NO: 30 in page 68 of the specification (AAE21142)
 XX
 SQ Sequence 84 AA;

Query Match 100.0%; Score 40; DB 5; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 25 TGEKPYK 31

RESULT 14

AAE38681

ID AAE38681 standard; protein; 84 AA.

XX

AC AAE38681;

XX

DT 04-DEC-2003 (first entry)

XX

DE Zinc finger protein #11.

XX

KW Artificial transcription factor; DNA binding protein; ATF; ZFP; therapy;
 KW zinc finger protein; crop protection; disease-resistant; transgenic;
 KW transgenic plant.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 15

FT /note= "Xaa = Any amino acid"

XX

PN WO2003062455-A2.

XX

PD 31-JUL-2003.

XX
 PF 23-JAN-2003; 2003WO-US002358.
 XX
 PR 23-JAN-2002; 2002US-00057408.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Sera T;
 XX
 DR WPI; 2003-646071/61.
 XX
 PT Preparing an artificial transcription factor (ATF) capable of modulating
 PT expression of a gene by interaction with a target site associated with
 PT the gene, for treating plant disease, comprises preparing a combinatorial
 PT library of ATFs.
 XX
 PS Example 4; Page 105; Opp; English.
 XX
 CC The invention relates to a method of preparing artificial transcription
 CC factor (ATF) capable of modulating expression of a gene by interaction
 CC with a target site associated with the gene. The method comprises
 CC preparing a combinatorial library of ATFs, each of the ATFs comprising a
 CC DNA-binding domain and a transcriptional regulatory domain. The invention
 CC also relates to DNA binding proteins comprising zinc finger domains and
 CC particularly to the identification of a context-independent recognition
 CC code to zinc finger domains. The methods are useful for treating disease
 CC in a plant, for crop protection and for producing genetically transformed
 CC disease-resistant plants. The present sequence is a zinc finger protein
 CC (ZFP)
 XX
 SQ Sequence 84 AA;

Query Match 100.0%; Score 40; DB 7; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 25 TGEKPYK 31

RESULT 15

ABP01014

ID ABP01014 standard; protein; 88 AA.

XX

AC ABP01014;

XX

DT 25-JUN-2002 (first entry)

XX

DE Human ORFX protein sequence SEQ ID NO:2010.

XX

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

KW degenerative disorder; osteoarthritis; neurodegenerative disorder;

KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW hypertension; hypothyroidism; cholesterol ester storage disease;

KW immune deficiency; immune disorder; infectious disease;

KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 XX
 OS Homo sapiens.
 XX
 PN WO200192523-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US010836.
 XX
 PR 30-MAY-2000; 2000US-0206132P.
 PR 29-AUG-2000; 2000US-0228716P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach MD;
 XX
 DR WPI; 2002-106308/14.
 DR N-PSDB; ABN16766.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX
 PS Disclosure; SEQ ID NO 2010; 1037pp; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 88 AA;

Query Match 100.0%; Score 40; DB 5; Length 88;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||||
Db 75 TGEKPYK 81

Search completed: March 5, 2004, 16:22:46
Job time : 8 secs

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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:17:14 ; Search time 1.87963 Seconds
(without alignments)
192.262 Million cell updates/sec

Title: US-10-057-890A-8
Perfect score: 40
Sequence: 1 TGEKPYK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	40	100.0	28	3	US-09-253-396A-220	Sequence 220, App
2	40	100.0	28	3	US-09-253-396A-222	Sequence 222, App
3	40	100.0	60	2	US-08-117-952-786	Sequence 786, App
4	40	100.0	98	4	US-09-229-007A-10	Sequence 10, Appl
5	40	100.0	100	4	US-09-989-789-15	Sequence 15, Appl
6	40	100.0	185	4	US-09-494-190-125	Sequence 125, App
7	40	100.0	185	4	US-09-494-190-126	Sequence 126, App
8	40	100.0	219	1	US-08-843-993-4	Sequence 4, Appli
9	40	100.0	219	3	US-09-059-520A-4	Sequence 4, Appli
10	40	100.0	219	3	US-09-334-275-4	Sequence 4, Appli
11	40	100.0	219	4	US-09-919-172-74	Sequence 74, Appl

12	40	100.0	313	4	US-09-800-729-196	Sequence 196, App
13	40	100.0	326	4	US-09-800-729-195	Sequence 195, App
14	40	100.0	344	1	US-08-843-993-3	Sequence 3, Appli
15	40	100.0	344	3	US-09-059-520A-3	Sequence 3, Appli
16	40	100.0	344	3	US-09-334-275-3	Sequence 3, Appli
17	40	100.0	345	1	US-08-843-993-1	Sequence 1, Appli
18	40	100.0	345	3	US-09-059-520A-1	Sequence 1, Appli
19	40	100.0	345	3	US-09-334-275-1	Sequence 1, Appli
20	40	100.0	368	2	US-08-933-750C-14	Sequence 14, Appl
21	40	100.0	368	3	US-09-234-613-14	Sequence 14, Appl
22	40	100.0	488	2	US-08-933-750C-17	Sequence 17, Appl
23	40	100.0	488	3	US-09-234-613-17	Sequence 17, Appl
24	40	100.0	518	4	US-09-881-578A-4	Sequence 4, Appli
25	40	100.0	640	3	US-09-262-773-4	Sequence 4, Appli
26	40	100.0	648	3	US-09-262-773-2	Sequence 2, Appli
27	40	100.0	711	2	US-08-820-170A-10	Sequence 10, Appl
28	40	100.0	711	3	US-09-055-699-10	Sequence 10, Appl
29	40	100.0	711	3	US-09-273-565-10	Sequence 10, Appl
30	40	100.0	711	4	US-09-565-538-10	Sequence 10, Appl
31	40	100.0	711	4	US-09-661-468-10	Sequence 10, Appl
32	40	100.0	711	4	US-09-976-165-10	Sequence 10, Appl
33	37	92.5	41	4	US-09-389-831-15	Sequence 15, Appl
34	37	92.5	676	2	US-08-398-590A-40	Sequence 40, Appl
35	37	92.5	676	3	US-08-894-997-40	Sequence 40, Appl
36	37	92.5	706	1	US-08-074-967-2	Sequence 2, Appli
37	37	92.5	706	2	US-08-553-541B-2	Sequence 2, Appli
38	37	92.5	706	3	US-09-268-202-2	Sequence 2, Appli
39	37	92.5	706	5	PCT-US94-06669-2	Sequence 2, Appli
40	37	92.5	717	4	US-09-881-578A-2	Sequence 2, Appli
41	37	92.5	976	3	US-08-894-997-50	Sequence 50, Appl
42	36	90.0	28	3	US-09-253-396A-221	Sequence 221, App
43	36	90.0	28	3	US-09-253-396A-223	Sequence 223, App
44	36	90.0	28	3	US-09-253-396A-224	Sequence 224, App
45	36	90.0	28	3	US-09-253-396A-225	Sequence 225, App

ALIGNMENTS

RESULT 1

US-09-253-396A-220

; Sequence 220, Application US/09253396A

; Patent No. 6205404

; GENERAL INFORMATION:

; APPLICANT: Genome Dynamics, Inc.

; TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Class

; FILE REFERENCE: 1116242-0003 file: genome03F.app

; CURRENT APPLICATION NUMBER: US/09/253,396A

; CURRENT FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 231

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 220

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-253-396A-220

Query Match 100.0%; Score 40; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | | |
Db 1 TGEKPYK 7

RESULT 2

US-09-253-396A-222
; Sequence 222, Application US/09253396A
; Patent No. 6205404
; GENERAL INFORMATION:
; APPLICANT: Genome Dynamics, Inc.
; TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Class
; FILE REFERENCE: 1116242-0003 file: genome03F.app
; CURRENT APPLICATION NUMBER: US/09/253,396A
; CURRENT FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-253-396A-222

Query Match 100.0%; Score 40; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | | |
Db 1 TGEKPYK 7

RESULT 3

US-08-117-952-786
; Sequence 786, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 786:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-117-952-786

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Query Match          100.0%; Score 40; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

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Qy      1 TGEKPYK 7
        |||||
Db      9 TGEKPYK 15

```

RESULT 4

```

US-09-229-007A-10
; Sequence 10, Application US/09229007A
; Patent No. 6453242
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselected Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/09/229,007A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence:Sp-1
; OTHER INFORMATION: transcription factor consensus sequence
US-09-229-007A-10

Query Match 100.0%; Score 40; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 68 TGEKPYK 74

RESULT 5

US-09-989-789-15

; Sequence 15, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sp-1 consensus
; OTHER INFORMATION: sequence
US-09-989-789-15

Query Match 100.0%; Score 40; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 68 TGEKPYK 74

RESULT 6

US-09-494-190-125

; Sequence 125, Application US/09494190
; Patent No. 6610512
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: TSRI 645.2
; CURRENT APPLICATION NUMBER: US/09/494,190
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: EP/99/07742
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: US 09/173,941

; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expressed
US-09-494-190-125

Query Match 100.0%; Score 40; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 36 TGEKPYK 42

RESULT 7

US-09-494-190-126

; Sequence 126, Application US/09494190
; Patent No. 6610512
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: TSRI 645.2
; CURRENT APPLICATION NUMBER: US/09/494,190
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: EP/99/07742
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: US 09/173,941
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expressed
US-09-494-190-126

Query Match 100.0%; Score 40; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 36 TGEKPYK 42

RESULT 8

US-08-843-993-4

; Sequence 4, Application US/08843993
; Patent No. 5739010

```

; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Shah, Purvi
;   TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/843,993
;     FILING DATE: Filed Herewith
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0274 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 219 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;       LIBRARY: GenBank
;       CLONE: 303597
US-08-843-993-4

```

```

Query Match          100.0%; Score 40; DB 1; Length 219;
Best Local Similarity 100.0%; Pred. No. 1;
Matches      7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      160 TGEKPYK 166

```

```

RESULT 9
US-09-059-520A-4
; Sequence 4, Application US/09059520A
; Patent No. 6001971
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Shah, Purvi

```

```

; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,520A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0274 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 303597
US-09-059-520A-4

```

```

Query Match          100.0%; Score 40; DB 3; Length 219;
Best Local Similarity 100.0%; Pred. No. 1;
Matches      7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      160 TGEKPYK 166

```

RESULT 10

US-09-334-275-4

```

; Sequence 4, Application US/09334275
; Patent No. 6037132
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,275
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/059,520
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0274 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 303597
US-09-334-275-4

```

```

Query Match          100.0%; Score 40; DB 3; Length 219;
Best Local Similarity 100.0%; Pred. No. 1;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      160 TGEKPYK 166

```

```

RESULT 11
US-09-919-172-74
; Sequence 74, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28

```

; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 74
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 021667CD1
US-09-919-172-74

Query Match 100.0%; Score 40; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 160 TGEKPYK 166

RESULT 12

US-09-800-729-196
; Sequence 196, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-196

Query Match 100.0%; Score 40; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 35 TGEKPYK 41

RESULT 13

US-09-800-729-195
; Sequence 195, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.

```
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 195
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-195
```

```
Query Match          100.0%; Score 40; DB 4; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches      7; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          1 TGEKPYK 7
             |||||
Db          48 TGEKPYK 54
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RESULT 14

US-08-843-993-3

```
; Sequence 3, Application US/08843993
; Patent No. 5739010
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Shah, Purvi
;   TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/843,993
;   FILING DATE: Filed Herewith
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0274 US
;   TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1244515
US-08-843-993-3

Query Match 100.0%; Score 40; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 284 TGEKPYK 290

RESULT 15

US-09-059-520A-3

; Sequence 3, Application US/09059520A
; Patent No. 6001971
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,520A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0274 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1244515
US-09-059-520A-3

Query Match 100.0%; Score 40; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 284 TGEKPYK 290

Search completed: March 5, 2004, 16:30:35
Job time : 1.87963 secs

OM protein - protein search, using sw model

Run on: March 5, 2004, 16:16:19 ; Search time 1.59877 Seconds
(without alignments)
421.163 Million cell updates/sec

Title: US-10-057-890A-8
Perfect score: 40
Sequence: 1 TGEKPYK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	40	100.0	29	2	F42075	finger protein (cl
2	40	100.0	53	2	D42075	finger protein (cl
3	40	100.0	55	2	I45193	zinc finger protei
4	40	100.0	56	2	I37973	zinc finger protei
5	40	100.0	56	2	I37976	zinc finger protei
6	40	100.0	57	2	E42075	finger protein (cl
7	40	100.0	57	2	B43284	zinc finger protei
8	40	100.0	60	2	C42075	finger protein (cl
9	40	100.0	66	2	S47065	finger protein HZF
10	40	100.0	88	2	D43284	finger protein ZNF
11	40	100.0	91	2	H42075	finger protein (cl
12	40	100.0	93	2	PQ0636	zinc finger protei
13	40	100.0	102	2	G45193	zinc finger protei

14	40	100.0	106	2	T34560	hypothetical prote
15	40	100.0	107	2	I39315	zinc-finger protei
16	40	100.0	109	2	H45193	zinc finger protei
17	40	100.0	149	2	A29942	developmental cont
18	40	100.0	156	2	B45447	zinc finger (alter
19	40	100.0	169	2	S47066	finger protein HZF
20	40	100.0	169	2	A39240	finger protein mfg
21	40	100.0	183	2	S70007	finger protein zfo
22	40	100.0	200	2	S47067	finger protein HZF
23	40	100.0	207	2	I38602	zinc finger protei
24	40	100.0	209	2	S47068	finger protein HZF
25	40	100.0	219	2	S35643	BTEB2 protein - hu
26	40	100.0	225	2	T26491	hypothetical prote
27	40	100.0	229	2	A48927	Kruppel-like zinc
28	40	100.0	232	2	T12490	hypothetical prote
29	40	100.0	239	2	I38615	zinc finger protei
30	40	100.0	247	2	S47070	finger protein HZF
31	40	100.0	261	2	S70006	finger protein zfo
32	40	100.0	280	2	S06572	finger protein (cl
33	40	100.0	289	2	A48913	KRAB zinc finger p
34	40	100.0	296	2	A45447	zinc finger (alter
35	40	100.0	308	2	A44496	transcription repr
36	40	100.0	319	2	T46469	hypothetical prote
37	40	100.0	344	2	JC6100	CACCC-box binding
38	40	100.0	347	2	S00549	developmental cont
39	40	100.0	383	2	C32891	finger protein 9,
40	40	100.0	401	2	A42177	KRAB-domain-contai
41	40	100.0	411	2	S10245	finger protein, te
42	40	100.0	415	2	S34140	DNA-binding protei
43	40	100.0	415	2	S37690	DNA-binding protei
44	40	100.0	420	2	S06579	finger protein (cl
45	40	100.0	427	2	A35659	krueppel-related p

ALIGNMENTS

RESULT 1

F42075

finger protein (clone ZnFP30) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 01-Dec-2000

C;Accession: F42075

R;Hoovers, J.M.N.; Mannens, M.; John, R.; Blik, J.; van Heyningen, V.;

Porteous, D.J.; Leschot, N.J.; Westerveld, A.; Little, P.F.R.

Genomics 12, 254-263, 1992

A;Title: High-resolution localization of 69 potential human zinc finger protein genes: a number are clustered.

A;Reference number: A42075; MUID:92155714; PMID:1740334

A;Accession: F42075

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-29 <HOO>

C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match

100.0%; Score 40; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 16 TGEKPYK 22

RESULT 2

D42075

finger protein (clone ZnFP19) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999

C;Accession: D42075

R;Hoovers, J.M.N.; Mannens, M.; John, R.; Blik, J.; van Heyningen, V.;

Porteous, D.J.; Leschot, N.J.; Westerveld, A.; Little, P.F.R.

Genomics 12, 254-263, 1992

A;Title: High-resolution localization of 69 potential human zinc finger protein genes: a number are clustered.

A;Reference number: A42075; MUID:92155714; PMID:1740334

A;Accession: D42075

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-53 <HOO>

Query Match 100.0%; Score 40; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 40 TGEKPYK 46

RESULT 3

I45193

zinc finger protein ZNF66 (C2-H2 zinc finger motif) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C;Accession: I45193

R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.

Genomics 13, 999-1007, 1992

A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile site regions of human chromosomes.

A;Reference number: A43284; MUID:92372070; PMID:1505991

A;Accession: I45193

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-55 <LIC>

A;Cross-references: GB:M88375; NID:g340487; PIDN:AAA61333.1; PID:g553818

A;Note: sequence extracted from NCBI backbone (NCBIN:111683, NCBIP:111684)

C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 100.0%; Score 40; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 12 TGEKPYK 18

RESULT 4

I37973

zinc finger protein kox5 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 01-Dec-2000

C;Accession: I37973; S10422

R;Thiesen, H.J.

New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288909

A;Accession: I37973

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-56 <RES>

A;Cross-references: EMBL:X52336; NID:g34166; PIDN:CAA36562.1; PID:g930096

C;Genetics:

A;Gene: GDB:ZNF13

A;Cross-references: GDB:125320; OMIM:194554

A;Map position: 19q13.2-19qter

C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 40; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 24 TGEKPYK 30

RESULT 5

I37976

zinc finger protein kox8 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 01-Dec-2000

C;Accession: I37976; S10425

R;Thiesen, H.J.

New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288909

A;Accession: I37976

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-56 <RES>

A;Cross-references: EMBL:X52339; NID:g34169; PIDN:CAA36565.1; PID:g930099

C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 40; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 24 TGEKPYK 30

RESULT 6

E42075

finger protein (clone ZnFP29) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999

C;Accession: E42075

R;Hoovers, J.M.N.; Mannens, M.; John, R.; Blik, J.; van Heyningen, V.;

Porteous, D.J.; Leschot, N.J.; Westerveld, A.; Little, P.F.R.

Genomics 12, 254-263, 1992

A;Title: High-resolution localization of 69 potential human zinc finger protein genes: a number are clustered.

A;Reference number: A42075; MUID:92155714; PMID:1740334

A;Accession: E42075

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-57 <HOO>

Query Match 100.0%; Score 40; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 44 TGEKPYK 50

RESULT 7

B43284

zinc finger protein ZNF48 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: B43284

R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.

Genomics 13, 999-1007, 1992

A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile site regions of human chromosomes.

A;Reference number: A43284; MUID:92372070; PMID:1505991

A;Accession: B43284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-57 <LIC>

A;Cross-references: GB:M88358; NID:g340451; PIDN:AAA61316.1; PID:g340452

A;Note: sequence extracted from NCBI backbone (NCBIN:111632, NCBIP:111633)

Query Match 100.0%; Score 40; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 10 TGEKPYK 16

RESULT 8

C42075

finger protein (clone ZnFP12) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999

C;Accession: C42075

R;Hoovers, J.M.N.; Mannens, M.; John, R.; Bliek, J.; van Heyningen, V.;

Porteous, D.J.; Leschot, N.J.; Westerveld, A.; Little, P.F.R.

Genomics 12, 254-263, 1992

A;Title: High-resolution localization of 69 potential human zinc finger protein genes: a number are clustered.

A;Reference number: A42075; MUID:92155714; PMID:1740334

A;Accession: C42075

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-60 <HOO>

Query Match 100.0%; Score 40; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 31 TGEKPYK 37

RESULT 9

S47065

finger protein HZF7, Krueppel-related - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000

C;Accession: S47065; I37573

R;Abrink, M.; Aveskogh, M.; Hellman, L.

submitted to the EMBL Data Library, June 1994

A;Description: Isolation of cDNA clones for 42 different Krueppel-related zinc finger proteins encoded by the human genome.

A;Reference number: S47065

A;Accession: S47065

A;Molecule type: mRNA

A;Residues: 1-66 <ABR>

R;Abrink, M.; Aveskogh, M.; Hellman, L.

DNA Cell Biol. 14, 125-136, 1995

A;Title: Isolation of cDNA clones for 42 different Kruppel-related zinc finger proteins expressed in the human monoblast cell line U-937.

A;Reference number: I37566; MUID:95169271; PMID:7865130

A;Accession: I37573

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-66 <RES>

A;Cross-references: EMBL:X78930; NID:g498732; PIDN:CAA55530.1; PID:g836629

C;Genetics:
A;Gene: HZF7
C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 40; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 12 TGEKPYK 18

RESULT 10

D43284

finger protein ZNF50 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

C;Accession: D43284

R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.

Genomics 13, 999-1007, 1992

A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile site regions of human chromosomes.

A;Reference number: A43284; MUID:92372070; PMID:1505991

A;Accession: D43284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-88 <LIC>

A;Cross-references: GB:M88360; NID:g340457; PID:g340458

A;Note: sequence extracted from NCBI backbone (NCBIN:111638, NCBIP:111639)

C;Keywords: zinc finger

Query Match 100.0%; Score 40; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 34 TGEKPYK 40

RESULT 11

H42075

finger protein (clone ZnFP39) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999

C;Accession: H42075

R;Hoovers, J.M.N.; Mannens, M.; John, R.; Bliek, J.; van Heyningen, V.;

Porteous, D.J.; Leschot, N.J.; Westerveld, A.; Little, P.F.R.

Genomics 12, 254-263, 1992

A;Title: High-resolution localization of 69 potential human zinc finger protein genes: a number are clustered.

A;Reference number: A42075; MUID:92155714; PMID:1740334

A;Accession: H42075

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-91 <HOO>

Query Match 100.0%; Score 40; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 50 TGEKPYK 56

RESULT 12

PQ0636

zinc finger protein CZF - human (fragment)

N;Alternate names: cerebellar zinc finger protein

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 10-May-1996

C;Accession: PQ0636

R;Sato, S.; Inuzuka, T.; Nakano, R.; Fujita, N.; Matsubara, N.; Sakimura, K.;
Mishina, M.; Miyatake, T.

Biochem. Biophys. Res. Commun. 178, 198-206, 1991

A;Title: Antibody to a zinc finger protein in a patient with paraneoplastic
cerebellar degeneration.

A;Reference number: PQ0636; MUID:91298948; PMID:1712585

A;Accession: PQ0636

A;Molecule type: mRNA

A;Residues: 1-93 <SAT>

A;Experimental source: cerebellum

C;Keywords: zinc finger

Query Match 100.0%; Score 40; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 73 TGEKPYK 79

RESULT 13

G45193

zinc finger protein ZNF64 (C2-H2 zinc finger motif) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

C;Accession: G45193

R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.

Genomics 13, 999-1007, 1992

A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and
fragile site regions of human chromosomes.

A;Reference number: A43284; MUID:92372070; PMID:1505991

A;Accession: G45193

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-102 <LIC>

A;Note: sequence extracted from NCBI backbone (NCBIN:111675, NCBIP:111679)

Query Match 100.0%; Score 40; DB 2; Length 102;

Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 95 TGEKPYK 101

RESULT 14

T34560

hypothetical protein DKFZp434J0650.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T34560

R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, October 1999

A;Reference number: Z21540

A;Accession: T34560

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <POU>

A;Cross-references: EMBL:AL122078

A;Experimental source: adult testis; clone DKFZp434J0650

C;Genetics:

A;Note: DKFZp434J0650.1

Query Match 100.0%; Score 40; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 21 TGEKPYK 27

RESULT 15

I39315

zinc-finger protein (ZNFpT7) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999

C;Accession: I39315

R;Huebner, K.; Druck, T.; LaForgia, S.; Lasota, J.; Croce, C.M.; Lanfranccone,
L.; Donti, E.; Pengue, G.; La Mantia, G.; Pelicci, P.G.

Hum. Genet. 91, 217-222, 1993

A;Title: Chromosomal localization of four human zinc finger cDNAs.

A;Reference number: I39313; MUID:93239177; PMID:8478004

A;Accession: I39315

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-107 <RES>

A;Cross-references: EMBL:X65232; NID:g505547; PIDN:CAA46339.1; PID:g505548

Query Match 100.0%; Score 40; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7

Db |||||
 37 TGEKPYK 43

Search completed: March 5, 2004, 16:28:55
Job time : 1.59877 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2004, 16:22:54 ; Search time 3.78086 Seconds
(without alignments)
390.935 Million cell updates/sec

Title: US-10-057-890A-8
Perfect score: 40
Sequence: 1 TGEKPYK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length DB	ID			Description

1	40	100.0	7	14	US-10-057-890A-8	Sequence 8, Appli
2	40	100.0	34	9	US-09-785-632A-25	Sequence 25, Appl
3	40	100.0	46	14	US-10-029-386-29751	Sequence 29751, A
4	40	100.0	47	14	US-10-029-386-30721	Sequence 30721, A
5	40	100.0	48	14	US-10-029-386-29643	Sequence 29643, A
6	40	100.0	48	14	US-10-029-386-29844	Sequence 29844, A
7	40	100.0	51	14	US-10-029-386-29892	Sequence 29892, A
8	40	100.0	52	14	US-10-029-386-29011	Sequence 29011, A
9	40	100.0	53	14	US-10-029-386-28629	Sequence 28629, A
10	40	100.0	71	14	US-10-029-386-28469	Sequence 28469, A
11	40	100.0	73	9	US-09-867-550-2018	Sequence 2018, Ap
12	40	100.0	79	14	US-10-029-386-28542	Sequence 28542, A
13	40	100.0	79	14	US-10-029-386-33598	Sequence 33598, A
14	40	100.0	84	10	US-09-911-261A-30	Sequence 30, Appl
15	40	100.0	84	14	US-10-057-408-30	Sequence 30, Appl
16	40	100.0	90	14	US-10-209-194-10	Sequence 10, Appl
17	40	100.0	90	14	US-10-147-286-5	Sequence 5, Appli
18	40	100.0	90	14	US-10-303-686A-5	Sequence 5, Appli
19	40	100.0	90	15	US-10-395-816A-5	Sequence 5, Appli
20	40	100.0	96	14	US-10-029-386-32050	Sequence 32050, A
21	40	100.0	98	14	US-10-113-424-10	Sequence 10, Appl
22	40	100.0	99	10	US-09-911-261A-5	Sequence 5, Appli
23	40	100.0	99	10	US-09-911-261A-6	Sequence 6, Appli
24	40	100.0	99	10	US-09-911-261A-7	Sequence 7, Appli
25	40	100.0	99	10	US-09-911-261A-8	Sequence 8, Appli
26	40	100.0	99	10	US-09-911-261A-9	Sequence 9, Appli
27	40	100.0	99	10	US-09-911-261A-10	Sequence 10, Appl
28	40	100.0	99	14	US-10-057-408-5	Sequence 5, Appli
29	40	100.0	99	14	US-10-057-408-6	Sequence 6, Appli
30	40	100.0	99	14	US-10-057-408-7	Sequence 7, Appli
31	40	100.0	99	14	US-10-057-408-8	Sequence 8, Appli
32	40	100.0	99	14	US-10-057-408-9	Sequence 9, Appli
33	40	100.0	99	14	US-10-057-408-10	Sequence 10, Appl
34	40	100.0	99	14	US-10-029-386-30335	Sequence 30335, A
35	40	100.0	100	9	US-09-989-789-15	Sequence 15, Appl
36	40	100.0	100	10	US-09-846-033B-223	Sequence 223, App
37	40	100.0	100	10	US-09-990-186-15	Sequence 15, Appl
38	40	100.0	100	10	US-09-989-994-15	Sequence 15, Appl
39	40	100.0	100	14	US-10-006-069A-223	Sequence 223, App
40	40	100.0	104	9	US-09-764-864-1324	Sequence 1324, Ap
41	40	100.0	104	9	US-09-764-864-1382	Sequence 1382, Ap
42	40	100.0	104	15	US-10-074-024-352	Sequence 352, App
43	40	100.0	109	11	US-09-864-408A-5572	Sequence 5572, Ap
44	40	100.0	111	9	US-09-764-864-1502	Sequence 1502, Ap
45	40	100.0	111	10	US-09-764-891-4219	Sequence 4219, Ap

ALIGNMENTS

RESULT 1
 US-10-057-890A-8
 ; Sequence 8, Application US/10057890A
 ; Publication No. US20030044901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coleman, Timothy

```

; APPLICANT: Mansfield, Brian
; TITLE OF INVENTION: Scaffold Fusion Polypeptides, Composition for Making the
Same, and Methods
; TITLE OF INVENTION: of Using the Same.
; FILE REFERENCE: PF537
; CURRENT APPLICATION NUMBER: US/10/057,890A
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/265,782
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,858
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-890A-8

```

```

Query Match          100.0%; Score 40; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches      7; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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```

Qy      1 TGEKPYK 7
        |||||
Db      1 TGEKPYK 7

```

RESULT 2

```

US-09-785-632A-25
; Sequence 25, Application US/09785632A
; Patent No. US20020061512A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Kwon, Young Do
; APPLICANT: Kim, Hyun-Won
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAINS AND METHODS OF
; TITLE OF INVENTION: IDENTIFYING SAME
; FILE REFERENCE: 12279-002001
; CURRENT APPLICATION NUMBER: US/09/785,632A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-632A-25

```

```

Query Match          100.0%; Score 40; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches      7; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      1 TGEKPYK 7

```

RESULT 3

US-10-029-386-29751

; Sequence 29751, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29751
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: P51522, EVALUATE 6.00e-19
US-10-029-386-29751

Query Match 100.0%; Score 40; DB 14; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
Db 6 TGEKPYK 12

RESULT 4

US-10-029-386-30721

; Sequence 30721, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

```

; SEQ ID NO 30721
;   LENGTH: 47
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR19.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.8
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
;   OTHER INFORMATION: SWISSPROT HIT: Q03923, EVALUE 3.00e-24
US-10-029-386-30721

```

```

Query Match          100.0%; Score 40; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches      7; Conservative      0; Mismatches      0; Indels      0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      4 TGEKPYK 10

```

RESULT 5

US-10-029-386-29643

; Sequence 29643, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 29643

; LENGTH: 48

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR18.1

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.7

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.75

; OTHER INFORMATION: SWISSPROT HIT: Q14586, EVALUE 1.00e-19
US-10-029-386-29643

```

Query Match          100.0%; Score 40; DB 14; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 TGEKPYK 7

```


Db

|||||||
6 TGEKPYK 12

RESULT 6

US-10-029-386-29844

; Sequence 29844, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29844
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.46
; OTHER INFORMATION: SWISSPROT HIT: Q14584, EVALUE 1.00e-22
US-10-029-386-29844

Query Match 100.0%; Score 40; DB 14; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 6 TGEKPYK 12

RESULT 7

US-10-029-386-29892

; Sequence 29892, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288

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; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29892
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76
; OTHER INFORMATION: SWISSPROT HIT: Q9NYT6, EVALUE 1.00e-26
US-10-029-386-29892

```

```

Query Match          100.0%; Score 40; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches      7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      11 TGEKPYK 17

```

RESULT 8

```

US-10-029-386-29011
; Sequence 29011, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29011
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.44
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: Q9UL59, EVALUE 7.00e-20
US-10-029-386-29011

```

```

Query Match          100.0%; Score 40; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches      7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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Qy 1 TGEKPYK 7
|||
Db 22 TGEKPYK 28

RESULT 9

US-10-029-386-28629
; Sequence 28629, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28629
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P17024, EVALUE 6.00e-22
US-10-029-386-28629

Query Match 100.0%; Score 40; DB 14; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||
Db 9 TGEKPYK 15

RESULT 10

US-10-029-386-28469
; Sequence 28469, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE

```

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28469
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.9
; OTHER INFORMATION: SWISSPROT HIT: Q15776, EVALUE 2.00e-40
US-10-029-386-28469

```

```

Query Match          100.0%; Score 40; DB 14; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      33 TGEKPYK 39

```

```

RESULT 11
US-09-867-550-2018
; Sequence 2018, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic
Cells and Polypeptides Encoded
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2018
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-2018

```

Query Match 100.0%; Score 40; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
Db 17 TGEKPYK 23

RESULT 12

US-10-029-386-28542
; Sequence 28542, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28542
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
; OTHER INFORMATION: SWISSPROT HIT: Q9Y2Q1, EVALUE 4.00e-38
US-10-029-386-28542

Query Match 100.0%; Score 40; DB 14; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
Db 7 TGEKPYK 13

RESULT 13

US-10-029-386-33598
; Sequence 33598, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.

```

; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33598
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: SWISSPROT HIT: Q61116, EVALUE 1.00e-41
US-10-029-386-33598

```

```

Query Match          100.0%; Score 40; DB 14; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      5 TGEKPYK 11

```

RESULT 14

```

US-09-911-261A-30
; Sequence 30, Application US/09911261A
; Publication No. US20030134350A1
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Zinc finger protein
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (15)..(15)
; OTHER INFORMATION: Amino acid 15 is "Xaa" wherein "Xaa" = is any amino acid.
US-09-911-261A-30

```

```

Query Match          100.0%; Score 40; DB 10; Length 84;

```

Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||
Db 25 TGEKPYK 31

RESULT 15

US-10-057-408-30

; Sequence 30, Application US/10057408

; Publication No. US20030082561A1

; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135

; CURRENT APPLICATION NUMBER: US/10/057,408

; CURRENT FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060

; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 30

; LENGTH: 84

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Zinc finger protein

; NAME/KEY: VARIANT

; LOCATION: (15)..(15)

; OTHER INFORMATION: Amino acid 15 is "Xaa" wherein "Xaa" = is any amino acid.
US-10-057-408-30

Query Match 100.0%; Score 40; DB 14; Length 84;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||
Db 25 TGEKPYK 31

Search completed: March 5, 2004, 16:33:43

Job time : 4.78086 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2004, 16:15:44 ; Search time 4.64506 Seconds
(without alignments)
475.479 Million cell updates/sec

Title: US-10-057-890A-8
Perfect score: 40
Sequence: 1 TGEKPYK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	40	100.0	32	11	Q9QWN2	Q9qwn2 mus musculu
2	40	100.0	36	11	P97650	P97650 rattus norv
3	40	100.0	50	4	O60862	O60862 homo sapien
4	40	100.0	55	4	Q15939	Q15939 homo sapien
5	40	100.0	57	4	Q15920	Q15920 homo sapien
6	40	100.0	57	11	O88234	O88234 mus musculu
7	40	100.0	57	11	Q9QWM9	Q9qwm9 mus musculu
8	40	100.0	57	11	Q9QWM7	Q9qwm7 mus musculu
9	40	100.0	57	11	O88248	O88248 mus musculu
10	40	100.0	57	11	Q9QWN0	Q9qwn0 mus musculu
11	40	100.0	57	11	Q9QWM8	Q9qwm8 mus musculu
12	40	100.0	68	4	O14885	O14885 homo sapien
13	40	100.0	71	11	P97657	P97657 rattus norv
14	40	100.0	72	4	O14858	O14858 homo sapien
15	40	100.0	82	11	Q8BUB8	Q8bub8 mus musculu
16	40	100.0	85	11	O88258	O88258 mus musculu
17	40	100.0	85	11	O88253	O88253 mus musculu
18	40	100.0	85	11	O88251	O88251 mus musculu
19	40	100.0	85	11	O88249	O88249 mus musculu
20	40	100.0	85	11	O88255	O88255 mus musculu
21	40	100.0	85	11	O88256	O88256 mus musculu
22	40	100.0	85	11	O88250	O88250 mus musculu
23	40	100.0	88	4	Q15922	Q15922 homo sapien
24	40	100.0	92	11	Q8C2B8	Q8c2b8 mus musculu
25	40	100.0	96	11	Q8BZ72	Q8bz72 mus musculu
26	40	100.0	97	4	Q16524	Q16524 homo sapien
27	40	100.0	106	4	Q9UFH1	Q9ufh1 homo sapien
28	40	100.0	107	11	Q60916	Q60916 mus musculu
29	40	100.0	109	4	Q15938	Q15938 homo sapien
30	40	100.0	121	4	Q8NB48	Q8nb48 homo sapien
31	40	100.0	122	11	Q8BSG2	Q8bsg2 mus musculu
32	40	100.0	129	4	Q9H963	Q9h963 homo sapien
33	40	100.0	130	6	Q95286	Q95286 sus scrofa
34	40	100.0	130	11	Q60913	Q60913 mus musculu
35	40	100.0	138	11	Q8BIW3	Q8biw3 mus musculu
36	40	100.0	139	4	Q8N229	Q8n229 homo sapien
37	40	100.0	145	4	Q9NZ00	Q9nz00 homo sapien
38	40	100.0	149	11	Q61778	Q61778 mus musculu
39	40	100.0	164	6	Q7YR90	Q7yr90 bos taurus
40	40	100.0	167	4	Q9H3U2	Q9h3u2 homo sapien
41	40	100.0	167	4	Q8NCC0	Q8ncc0 homo sapien
42	40	100.0	169	4	Q96IL9	Q96il9 homo sapien
43	40	100.0	173	4	Q9H9X5	Q9h9x5 homo sapien
44	40	100.0	184	4	Q15914	Q15914 homo sapien
45	40	100.0	202	4	Q92970	Q92970 homo sapien

ALIGNMENTS

RESULT 1

Q9QWN2

ID Q9QWN2 PRELIMINARY; PRT; 32 AA.

AC Q9QWN2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Mszf68 (Fragment).
 GN MSZF68.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR.";
 RL Gene 213:55-64(1998).
 DR EMBL; AB010314; BAA31370.1; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR ProDom; PD000003; Znf_C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 32 32
 SQ SEQUENCE 32 AA; 3610 MW; 8E1CDDE3F766B6E4 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 3 TGEKPYK 9

RESULT 2

P97650

ID P97650 PRELIMINARY; PRT; 36 AA.
 AC P97650;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Zinc finger protein 11 (Fragment).
 GN AZF11.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96220733; PubMed=8635150;
 RA Mesa K., Gebelein B., Cook T., Urrutia R.;
 RT "Identification and characterization of zinc finger encoding genes
 RT from the tumoral exocrine pancreatic cell line AR42J.";
 RL Cancer Lett. 103:143-149(1996).
 DR EMBL; U78122; AAB36794.1; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.

DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
FT NON_TER 1 1
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 4006 MW; 945DA8F9E1A3F366 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 23 TGEKPYK 29

RESULT 3

O60862

ID O60862 PRELIMINARY; PRT; 50 AA.
AC O60862;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Zinc finger protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Rosbottom J., Newton D.J., Flanagan B.F.;
RT "Degenerate RT-PCR of zinc-finger domain mRNA in human fetal thymus.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ004948; CAA06236.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
FT NON_TER 1 1
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5989 MW; 9465A63107FE1439 CRC64;

Query Match 100.0%; Score 40; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 19 TGEKPYK 25

RESULT 4

Q15939

ID Q15939 PRELIMINARY; PRT; 55 AA.
 AC Q15939;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE DNA-binding protein (Fragment).
 GN ZNF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92052132; PubMed=1946370;
 RA Bray P., Lichter P., Thiesen H.J., Ward D.C., Dawid I.B.;
 RT "Characterization and mapping of human genes encoding zinc finger
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9563-9567(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92372070; PubMed=1505991;
 RA Lichter P., Bray P., Ried T., Dawid I.B., Ward D.C.;
 RT "Clustering of C2-H2 zinc finger motif sequences within telomeric and
 RT fragile site regions of human chromosomes.";
 RL Genomics 13:999-1007(1992).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; M88375; AAA61333.1; -.
 DR PIR; I45193; I45193.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 1.
 DR SMART; SM00355; ZnF_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc; Zinc-finger.
 FT NON TER 1 1
 SQ SEQUENCE 55 AA; 6322 MW; B3AD3100A4163ED5 CRC64;

Query Match 100.0%; Score 40; DB 4; Length 55;

Best Local Similarity 100.0%; Pred. No. 0.53;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGEKPYK 7
 |||||
 Db 12 TGEKPYK 18

RESULT 5

Q15920

ID Q15920 PRELIMINARY; PRT; 57 AA.

AC Q15920;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE DNA-binding protein (Fragment).
 GN ZNF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92052132; PubMed=1946370;
 RA Bray P., Lichter P., Thiesen H.J., Ward D.C., Dawid I.B.;
 RT "Characterization and mapping of human genes encoding zinc finger
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9563-9567(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92372070; PubMed=1505991;
 RA Lichter P., Bray P., Ried T., Dawid I.B., Ward D.C.;
 RT "Clustering of C2-H2 zinc finger motif sequences within telomeric and
 RT fragile site regions of human chromosomes.";
 RL Genomics 13:999-1007(1992).
 DR EMBL; M88358; AAA61316.1; -.
 DR PIR; B43284; B43284.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00355; ZnF_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW DNA-binding; Metal-binding; Zinc; Zinc-finger.
 FT NON TER 1 1
 SQ SEQUENCE 57 AA; 6375 MW; 9A482948BAB9429A CRC64;

Query Match 100.0%; Score 40; DB 4; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 10 TGEKPYK 16

RESULT 6

O88234

ID O88234 PRELIMINARY; PRT; 57 AA.
 AC O88234;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mszf17 (Fragment).
 GN MSZF17.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR.";
 RL Gene 213:55-64(1998).
 DR EMBL; AB010331; BAA31387.1; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 2.
 DR PRINTS; PR00048; ZINCFINGER.
 DR SMART; SM00355; ZnF_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6653 MW; 5DD232D9D70334E1 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 27 TGEKPYK 33

RESULT 7

Q9QWM9

ID Q9QWM9 PRELIMINARY; PRT; 57 AA.
 AC Q9QWM9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mszf83 (Fragment).
 GN MSZF83.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR.";
 RL Gene 213:55-64(1998).
 DR EMBL; AB010341; BAA31397.1; -.
 DR HSSP; P08045; 1ZNF.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 2.

DR ProDom; PD0000003; Znf_C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6693 MW; B5DF655C2D1243B7 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 27 TGEKPYK 33

RESULT 8

Q9QWM7

ID Q9QWM7 PRELIMINARY; PRT; 57 AA.
 AC Q9QWM7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mszf92 (Fragment).
 GN MSZF92.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR."
 RL Gene 213:55-64(1998).
 DR EMBL; AB010356; BAA31412.1; -.
 DR HSSP; P08045; 1ZNF.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 2.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD0000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6789 MW; 88D5E406C437CA1E CRC64;

Query Match 100.0%; Score 40; DB 11; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 27 TGEKPYK 33

RESULT 9

O88248

ID O88248 PRELIMINARY; PRT; 57 AA.
 AC O88248;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mszf18 (Fragment).
 GN 2810426N06RIK OR MSZF18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR."
 RL Gene 213:55-64(1998).
 DR EMBL; AB010346; BAA31402.1; -.
 DR MGD; MGI:1914857; 2810426N06Rik.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 2.
 DR ProDom; PD0000003; Znf_C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6744 MW; 073F92C62EF18609 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 27 TGEKPYK 33

RESULT 10

Q9QWN0

ID Q9QWN0 PRELIMINARY; PRT; 57 AA.
 AC Q9QWN0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mszf28 (Fragment).

GN MSZF28.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR."
 RL Gene 213:55-64(1998).
 DR EMBL; AB010328; BAA31384.1; -.
 DR HSSP; P08047; 1SP2.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 2.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; ZnF_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6611 MW; D61698C3A649B8F6 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 27 TGEKPYK 33

RESULT 11

Q9QWM8

ID Q9QWM8 PRELIMINARY; PRT; 57 AA.
 AC Q9QWM8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mszf24 (Fragment).
 GN MSZF24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR."

RL Gene 213:55-64(1998).
 DR EMBL; AB010348; BAA31404.1; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 2.
 DR SMART; SM00355; ZnF_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6725 MW; BE37B9E7D1C7321F CRC64;

Query Match 100.0%; Score 40; DB 11; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 27 TGEKPYK 33

RESULT 12

O14885

ID O14885 PRELIMINARY; PRT; 68 AA.
 AC O14885;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Zinc finger protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Sun X., Yu L., Wu G., Liu S., Hu P., Zhang M., Jiang Y., Shouyuan S.;
 RT "Isolation of novel human genes coding zinc finger protein from brain
 RT tissue - according to the conservativity of zinc finger motif."
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 0:0-0(1997).
 DR EMBL; AF027140; AAB84019.1; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 2.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; ZnF_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 68 68
 SQ SEQUENCE 68 AA; 7989 MW; ED10681BB6651D6B CRC64;

Query Match 100.0%; Score 40; DB 4; Length 68;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 56 TGEKPYK 62

RESULT 13

P97657

ID P97657 PRELIMINARY; PRT; 71 AA.
AC P97657;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Zinc finger protein 1 (Fragment).
GN DZF1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96319713; PubMed=8697448;
RA Gebelein B., Mesa K., Urrutia R.;
RT "A novel profile of expressed sequence tags for zinc finger encoding
RT genes from the poorly differentiated exocrine pancreatic cell line
RT AR4IP.";
RL Cancer Lett. 105:225-231(1996).
DR EMBL; U78129; AAB36801.1; -.
DR HSSP; P15822; 1BBO.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF00096; zf-C2H2; 2.
DR PRINTS; PR00048; ZINCFINGER.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
KW Metal-binding; Zinc; Zinc-finger.
FT NON_TER 1 1
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8025 MW; C1AF9C878E4B1351 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 39 TGEKPYK 45

RESULT 14

O14858

ID O14858 PRELIMINARY; PRT; 72 AA.
AC O14858;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Zinc finger protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Wu G., Yu L., Sun X., Wu M., Fan Y., Jiang C., Zheng Q., Zhang Q.,
 RA Zhao S.;
 RT "Isolation and Cloning of Novel C2-H2 Type Zinc Finger Protein Gene in
 RT Human Liver Tissue.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF024706; AAB81096.1; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 2.
 DR ProDom; PD000003; Znf_C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Metal-binding; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 72 72
 SQ SEQUENCE 72 AA; 8601 MW; E5D6DC6EBCF56C8D CRC64;

Query Match 100.0%; Score 40; DB 4; Length 72;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 62 TGEKPYK 68

RESULT 15

Q8BUB8

ID Q8BUB8 PRELIMINARY; PRT; 82 AA.
 AC Q8BUB8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Kruppel-like factor 7 (Fragment).
 GN KLF7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).

DR EMBL; AK086122; BAC39615.1; -.
DR MGD; MGI:1935151; Klf7.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00355; ZnF_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
FT NON_TER 1 1
SQ SEQUENCE 82 AA; 9861 MW; 37DDA2BBE9573715 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | |
Db 24 TGEKPYK 30

Search completed: March 5, 2004, 16:27:29
Job time : 4.64506 secs

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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:15:14 ; Search time 0.950617 Seconds
 (without alignments)
 383.426 Million cell updates/sec

Title: US-10-057-890A-8
 Perfect score: 40
 Sequence: 1 TGEKPYK 7

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	40	100.0	56	1	ZN13_HUMAN	P17016 homo sapien
2	40	100.0	56	1	ZN15_HUMAN	P17019 homo sapien
3	40	100.0	107	1	ZN79_HUMAN	Q15937 homo sapien
4	40	100.0	169	1	Z160_HUMAN	Q14589 homo sapien
5	40	100.0	169	1	ZF58_MOUSE	P16372 mus musculu
6	40	100.0	200	1	Z266_HUMAN	Q14584 homo sapien
7	40	100.0	207	1	Z137_HUMAN	P52743 homo sapien
8	40	100.0	209	1	Z235_HUMAN	Q14590 homo sapien
9	40	100.0	224	1	ZN22_HUMAN	P17026 homo sapien
10	40	100.0	239	1	Z138_HUMAN	P52744 homo sapien
11	40	100.0	247	1	Z273_HUMAN	Q14593 homo sapien
12	40	100.0	273	1	ZN80_GORGO	P51503 gorilla gor
13	40	100.0	275	1	Z253_HUMAN	O75346 homo sapien
14	40	100.0	280	1	ZG46_XENLA	P18722 xenopus lae
15	40	100.0	289	1	ZN75_HUMAN	P51815 homo sapien
16	40	100.0	293	1	ZN80_MACMU	P51505 macaca mula
17	40	100.0	296	1	Z124_HUMAN	Q15973 homo sapien

18	40	100.0	301	1	KLF7_MOUSE	Q99jb0	mus musculu
19	40	100.0	302	1	KLF7_HUMAN	O75840	homo sapien
20	40	100.0	308	1	AEF1_DROME	P39413	drosophila
21	40	100.0	321	1	Z177_HUMAN	Q13360	homo sapien
22	40	100.0	335	1	Z396_HUMAN	Q96n95	homo sapien
23	40	100.0	344	1	KLF3_MOUSE	Q60980	mus musculu
24	40	100.0	345	1	KLF3_HUMAN	P57682	homo sapien
25	40	100.0	347	1	ZFP2_MOUSE	P08043	mus musculu
26	40	100.0	348	1	Z435_HUMAN	Q9h4t2	homo sapien
27	40	100.0	359	1	KLF8_HUMAN	O95600	homo sapien
28	40	100.0	368	1	ZN24_HUMAN	P17028	homo sapien
29	40	100.0	368	1	ZN24_MOUSE	Q91vn1	mus musculu
30	40	100.0	402	1	KLFC_HUMAN	Q9y4x4	homo sapien
31	40	100.0	402	1	KLFC_MOUSE	O35738	mus musculu
32	40	100.0	415	1	ZN12_MICSA	P38621	micropterus
33	40	100.0	418	1	Z117_HUMAN	Q03924	homo sapien
34	40	100.0	420	1	Z229_HUMAN	Q9ujw7	homo sapien
35	40	100.0	420	1	ZG58_XENLA	P18730	xenopus lae
36	40	100.0	423	1	ZNFE_HUMAN	Q9un33	homo sapien
37	40	100.0	428	1	ZN83_HUMAN	P51522	homo sapien
38	40	100.0	439	1	ZO28_XENLA	P18747	xenopus lae
39	40	100.0	446	1	KLF5_MOUSE	Q9z0z7	mus musculu
40	40	100.0	446	1	ZN70_HUMAN	Q9uc06	homo sapien
41	40	100.0	451	1	Z222_HUMAN	Q9uk12	homo sapien
42	40	100.0	456	1	ZN25_HUMAN	P17030	homo sapien
43	40	100.0	457	1	KLF5_HUMAN	Q13887	homo sapien
44	40	100.0	458	1	Z239_HUMAN	Q16600	homo sapien
45	40	100.0	463	1	Z331_HUMAN	Q9nqx6	homo sapien

ALIGNMENTS

RESULT 1

ZN13_HUMAN

ID ZN13_HUMAN STANDARD; PRT; 56 AA.
AC P17016;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 13 (Zinc finger protein KOX5) (Fragment).
GN ZNF13 OR KOX5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=91145339; PubMed=2288909;
RA Thiesen H.-J.;
RT "Multiple genes encoding zinc finger domains are expressed in human T
RT cells.";
RL New Biol. 2:363-374(1990).
CC !- FUNCTION: May function as a transcription factor.
CC !- SUBCELLULAR LOCATION: Nuclear (Potential).
CC !- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-

CC FINGER PROTEINS.

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CC -----

DR EMBL; X52336; CAA36562.1; -.
DR PIR; I37973; I37973.
DR Genew; HGNC:12913; ZNF13.
DR MIM; 194554; -.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF00096; zf-C2H2; 2.
DR PRINTS; PR00048; ZINCFINGER.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; ZnF_C2H2; 2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat.
FT NON_TER 1 1
FT ZN_FING 1 23 C2H2-TYPE.
FT ZN_FING 29 51 C2H2-TYPE.
FT NON_TER 56 56
SQ SEQUENCE 56 AA; 6274 MW; 88F0BD74EBF5BD09 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | | | | |
Db 24 TGEKPYK 30

RESULT 2

ZN15_HUMAN

ID ZN15_HUMAN STANDARD; PRT; 56 AA.
AC P17019;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 15 (Zinc finger protein KOX8) (Fragment).
GN ZNF15L1 OR ZNF15 OR KOX8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=91145339; PubMed=2288909;
RA Thiesen H.-J.;

RT "Multiple genes encoding zinc finger domains are expressed in human T
RT cells.";
RL New Biol. 2:363-374(1990).
CC -!- FUNCTION: May function as a transcription factor.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52339; CAA36565.1; -.
DR PIR; I37976; I37976.
DR Genew; HGNC:12945; ZNF15L1.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF00096; zf-C2H2; 2.
DR PRINTS; PR00048; ZINCFINGER.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat.
FT NON_TER 1 1
FT ZN_FING 1 23 C2H2-TYPE.
FT ZN_FING 29 51 C2H2-TYPE.
FT NON_TER 56 56
SQ SEQUENCE 56 AA; 6377 MW; 89B6D137AE98023E CRC64;

Query Match 100.0%; Score 40; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 24 TGEKPYK 30

RESULT 3

ZN79_HUMAN

ID ZN79_HUMAN STANDARD; PRT; 107 AA.
AC Q15937;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 79 (ZNFpT7) (Fragment).
GN ZNF79.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=93239177; PubMed=8478004;
 RA Huebner K., Druck T., LaForgia S., Lasota J., Croce C.M.,
 RA Lanfranccone L., Donti E., Pengue G., La Mantia G., Pelicci P.-G.,
 RA Lania L.;
 RT "Chromosomal localization of four human zinc finger cDNAs.";
 RL Hum. Genet. 91:217-222(1993).
 CC -!- FUNCTION: May be involved in transcriptional regulation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
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 CC -----
 DR EMBL; X65232; CAA46339.1; -.
 DR PIR; I39315; I39315.
 DR Genew; HGNC:13153; ZNF79.
 DR MIM; 194552; -.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR PRINTS; PR00048; ZINCFINGER.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 FT NON_TER 1 1
 FT ZN_FING <1 11 C2H2-TYPE.
 FT ZN_FING 17 36 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 42 64 C2H2-TYPE.
 FT ZN_FING 70 92 C2H2-TYPE.
 FT ZN_FING 98 >107 C2H2-TYPE.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11999 MW; 14A45C64CBD791B5 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGEKPYK 7
 |||||
 Db 37 TGEKPYK 43

RESULT 4
 Z160_HUMAN
 ID Z160_HUMAN STANDARD; PRT; 169 AA.
 AC Q14589;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein 160 (HZF5) (Fragment).
 GN ZNF160.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95169271; PubMed=7865130;
 RA Abrink M., Aveskogh M., Hellman L.;
 RT "Isolation of cDNA clones for 42 different Kruppel-related zinc finger
 RT proteins expressed in the human monoblast cell line U-937.";
 RL DNA Cell Biol. 14:125-136(1995).
 CC -!- FUNCTION: May be involved in transcriptional regulation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -----
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 CC -----
 DR EMBL; X78928; CAA55528.1; -.
 DR PIR; S47066; S47066.
 DR HSSP; P25490; 1UBD.
 DR Genew; HGNC:12948; ZNF160.
 DR MIM; 600398; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; ZnF_C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 6.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 FT NON_TER 1 1
 FT ZN_FING <1 11 C2H2-TYPE.
 FT ZN_FING 21 43 C2H2-TYPE.
 FT ZN_FING 49 71 C2H2-TYPE.
 FT ZN_FING 77 99 C2H2-TYPE.
 FT ZN_FING 105 127 C2H2-TYPE.
 FT ZN_FING 133 155 C2H2-TYPE (DEGENERATE).
 FT NON_TER 169 169
 SQ SEQUENCE 169 AA; 19290 MW; 26D4EB29A6EEAFC3 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 169;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7

|||||||
Db 128 TGEKPYK 134

RESULT 5

ZF58_MOUSE

ID ZF58_MOUSE STANDARD; PRT; 169 AA.
AC P16372;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Zinc finger protein 58 (Zfp-58) (Zinc finger protein Mfg-1)
DE (Fragment).
GN ZFP58 OR MFG-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Skeletal muscle;
RX MEDLINE=90083278; PubMed=2512579;
RA Passananti C., Felsani A., Caruso M., Amati P.;
RT "Mouse genes coding for 'zinc-finger'-containing proteins:
RT characterization and expression in differentiated cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9417-9421(1989).
CC -!- FUNCTION: May have a role during differentiation processes.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Liver; testis; and at considerably lower
CC levels in brain, spleen and heart.
CC -!- DEVELOPMENTAL STAGE: Expression is positively regulated upon
CC differentiation and is not related to the cell cycle.
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -----
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CC -----
DR EMBL; M28513; AAA39531.1; -.
DR PIR; A39240; A39240.
DR HSSP; P25490; 1UBD.
DR MGD; MGI:99205; Zfp58.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF00096; zf-C2H2; 6.
DR PRINTS; PR00048; ZINCFINGER.
DR SMART; SM00355; ZnF_C2H2; 6.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
KW Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein.
FT NON_TER 1 1
FT ZN_FING 8 30 C2H2-TYPE.

```

FT  ZN_FING      36      58      C2H2-TYPE.
FT  ZN_FING      64      86      C2H2-TYPE.
FT  ZN_FING      92     114      C2H2-TYPE.
FT  ZN_FING     120     142      C2H2-TYPE.
FT  ZN_FING     148    >169      C2H2-TYPE.
FT  NON_TER      169     169
SQ  SEQUENCE    169 AA;  19585 MW;  7F55256B1406CDA3 CRC64;

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Query Match          100.0%; Score 40; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 TGEKPYK 7
        |||||
Db      31 TGEKPYK 37

```

RESULT 6

Z266_HUMAN

ID Z266_HUMAN STANDARD; PRT; 200 AA.

AC Q14584;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Zinc finger protein 266 (Zinc finger protein HZF1) (Fragment).

GN ZNF266.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95169271; PubMed=7865130;

RA Abrink M., Aveskogh M., Hellman L.;

RT "Isolation of cDNA clones for 42 different Kruppel-related zinc finger
 RT proteins expressed in the human monoblast cell line U-937.";

RL DNA Cell Biol. 14:125-136(1995).

CC -!- FUNCTION: May function as a transcription factor.

CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.

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DR EMBL; X78924; CAA55524.1; -.

DR PIR; S47067; S47067.

DR HSSP; P08047; 1SP2.

DR Genew; HGNC:13059; ZNF266.

DR MIM; 604751; -.

DR InterPro; IPR007087; Znf_C2H2.

DR InterPro; IPR007086; Znf_C2H2_sub.

DR Pfam; PF00096; zf-C2H2; 7.
 DR PRINTS; PR00048; ZINCFINGER.
 DR SMART; SM00355; ZnF_C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat; Polymorphism.
 FT NON_TER 1 1
 FT ZN_FING 3 25 C2H2-TYPE.
 FT ZN_FING 31 53 C2H2-TYPE.
 FT ZN_FING 59 81 C2H2-TYPE.
 FT ZN_FING 87 109 C2H2-TYPE.
 FT ZN_FING 115 137 C2H2-TYPE.
 FT ZN_FING 143 165 C2H2-TYPE.
 FT ZN_FING 171 193 C2H2-TYPE.
 FT VARIANT 170 170 P -> L (in dbSNP:10515).
 FT /FTId=VAR_014828.
 SQ SEQUENCE 200 AA; 22706 MW; 8559525BA225C7DC CRC64;

Query Match 100.0%; Score 40; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 138 TGEKPYK 144

RESULT 7

Z137_HUMAN

ID Z137_HUMAN STANDARD; PRT; 207 AA.
 AC P52743;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein 137.
 GN ZNF137.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Insulinoma;
 RX MEDLINE=96044430; PubMed=7557990;
 RA Tommerup N., Vissing H.;
 RT "Isolation and fine mapping of 16 novel human zinc finger-encoding
 RT cDNAs identify putative candidate genes for developmental and
 RT malignant disorders.";
 RL Genomics 27:259-264(1995).
 CC -!- FUNCTION: May be involved in transcriptional regulation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.

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CC -----

DR EMBL; U09414; AAC50255.1; -.
DR PIR; I38602; I38602.
DR Genew; HGNC:12921; ZNF137.
DR MIM; 604079; -.
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 6.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 6.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat; Polymorphism.
FT ZN_FING 72 94 C2H2-TYPE.
FT ZN_FING 100 122 C2H2-TYPE (DEGENERATE).
FT ZN_FING 128 150 C2H2-TYPE (DEGENERATE).
FT ZN_FING 156 178 C2H2-TYPE.
FT ZN_FING 184 206 C2H2-TYPE.
FT VARIANT 181 181 Q -> H (in dbSNP:1802617).
FT /FTId=VAR_012025.
SQ SEQUENCE 207 AA; 24115 MW; 44581FE39D47AA7A CRC64;

Query Match 100.0%; Score 40; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
| | | | |
Db 39 TGEKPYK 45

RESULT 8

Z235_HUMAN

ID Z235_HUMAN STANDARD; PRT; 209 AA.
AC Q14590;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 235 (Zinc finger protein 93 homolog) (Zfp-93)
DE (Zinc finger protein HZF6) (Fragment).
GN ZNF235 OR ZFP93 OR ZNF270.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95169271; PubMed=7865130;
RA Abrink M., Aveskogh M., Hellman L.;
RT "Isolation of cDNA clones for 42 different Kruppel-related zinc finger
RT proteins expressed in the human monoblast cell line U-937.";

RL DNA Cell Biol. 14:125-136(1995).
 CC -!- FUNCTION: May function as a transcription factor.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
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 CC -----
 DR EMBL; X78929; CAA55529.1; -.
 DR PIR; S47068; S47068.
 DR HSSP; P25490; 1ZNM.
 DR Genew; HGNC:12866; ZNF235.
 DR MIM; 604749; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2; 7.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 6.
 DR SMART; SM00355; Znf_C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 FT NON TER 1 1
 FT ZN_FING 4 26 C2H2-TYPE.
 FT ZN_FING 32 54 C2H2-TYPE.
 FT ZN_FING 60 82 C2H2-TYPE.
 FT ZN_FING 88 110 C2H2-TYPE.
 FT ZN_FING 116 138 C2H2-TYPE.
 FT ZN_FING 144 166 C2H2-TYPE.
 FT ZN_FING 172 194 C2H2-TYPE.
 FT ZN_FING 200 >209 C2H2-TYPE.
 FT NON TER 209 209
 SQ SEQUENCE 209 AA; 23915 MW; 9C12DE06BC7FFC8E CRC64;

Query Match 100.0%; Score 40; DB 1; Length 209;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 27 TGEKPYK 33

RESULT 9

ZN22_HUMAN

ID ZN22_HUMAN STANDARD; PRT; 224 AA.
 AC P17026; Q96FM4;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Zinc finger protein 22 (Zinc finger protein KOX15).
 GN ZNF22 OR KOX15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93043304; PubMed=1421376;
 RA Wu B.Y., Hanley E.W., Turka L.A., Nabel G.J.;
 RT "Isolation of a cDNA clone encoding a zinc finger protein highly
 RT expressed in T-leukemia lines.";
 RL Blood 80:2571-2576(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood, and Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 132-224 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92052132; PubMed=1946370;
 RA Bray P.L., Lichter P., Thiesen H.-J., Ward D.C., Dawid I.B.;
 RT "Characterization and mapping of human genes encoding zinc finger
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9563-9567(1991).
 RN [4]
 RP SEQUENCE OF 139-194 FROM N.A.
 RC TISSUE=Lymphoid;
 RX MEDLINE=91145339; PubMed=2288909;
 RA Thiesen H.-J.;
 RT "Multiple genes encoding zinc finger domains are expressed in human T
 RT cells.";
 RL New Biol. 2:363-374(1990).
 CC -!- FUNCTION: May be involved in transcriptional regulation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.

```

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S50223; AAB24264.2; -.
DR EMBL; BC010642; AAH10642.1; -.
DR EMBL; BC053687; AAH53687.1; -.
DR EMBL; M77172; AAA36815.1; -.
DR EMBL; X52346; CAA36572.1; -.
DR PIR; A48927; A48927.
DR HSSP; P08046; 1A1G.
DR Genew; HGNC:13012; ZNF22.
DR MIM; 194529; -.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF00096; zf-C2H2; 5.
DR PRINTS; PR00048; ZINCFINGER.
DR ProDom; PD000003; Znf_C2H2; 3.
DR SMART; SM00355; Znf_C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
KW Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;
KW Nuclear protein; Repeat.
FT ZN_FING      55      77      C2H2-TYPE.
FT ZN_FING      83     105      C2H2-TYPE.
FT ZN_FING     111     133      C2H2-TYPE.
FT ZN_FING     139     161      C2H2-TYPE.
FT ZN_FING     167     189      C2H2-TYPE.
FT CONFLICT      31      31      Q -> E (IN REF. 1).
FT CONFLICT     216     224      GRKSVAGLR -> EGSLWLVSVKYRAF (IN REF. 1).
SQ SEQUENCE     224 AA;  25915 MW;  61BE158D2CEAEE19 CRC64;

```

```

Query Match          100.0%; Score 40; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 TGEKPYK 7
        |||||
Db      106 TGEKPYK 112

```

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RESULT 10
Z138_HUMAN
ID   Z138_HUMAN      STANDARD;          PRT;   239 AA.
AC   P52744;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Zinc finger protein 138 (Fragment).
GN   ZNF138.
OS   Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Insulinoma;
 RX MEDLINE=96044430; PubMed=7557990;
 RA Tommerup N., Vissing H.;
 RT "Isolation and fine mapping of 16 novel human zinc finger-encoding
 RT cDNAs identify putative candidate genes for developmental and
 RT malignant disorders.";
 RL Genomics 27:259-264(1995).
 CC -!- FUNCTION: May be involved in transcriptional regulation as a
 CC repressor.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.

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DR EMBL; U09847; AAC50263.1; -.
 DR PIR; I38615; I38615.
 DR Genew; HGNC:12922; ZNF138.
 DR MIM; 604080; -.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003700; F:transcription factor activity; NAS.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR SMART; SM00355; ZnF_C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat; Repressor.
 FT NON_TER 1 1
 FT ZN_FING 89 111 C2H2-TYPE.
 FT ZN_FING 117 139 C2H2-TYPE (DEGENERATE).
 FT ZN_FING 145 167 C2H2-TYPE (DEGENERATE).
 FT ZN_FING 173 195 C2H2-TYPE.
 FT NON_TER 239 239
 SQ SEQUENCE 239 AA; 27938 MW; C0CB1CEEE0AEBAE6 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 140 TGEKPYK 146

RESULT 11

Z273_HUMAN

ID Z273_HUMAN STANDARD; PRT; 247 AA.

AC Q14593;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Zinc finger protein 273 (Zinc finger protein HZF9) (Fragment).

GN ZNF273.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95169271; PubMed=7865130;

RA Abrink M., Aveskogh M., Hellman L.;

RT "Isolation of cDNA clones for 42 different Kruppel-related zinc finger proteins expressed in the human monoblast cell line U-937.";

RL DNA Cell Biol. 14:125-136(1995).

CC -!- FUNCTION: May function as a transcription factor.

CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

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 CC -----

DR EMBL; X78932; CAA55532.1; -.

DR PIR; S47070; S47070.

DR HSSP; P08047; 1SP2.

DR Genew; HGNC:13067; ZNF273.

DR MIM; 604756; -.

DR InterPro; IPR007087; Znf_C2H2.

DR InterPro; IPR007086; Znf_C2H2_sub.

DR Pfam; PF00096; zf-C2H2; 7.

DR PRINTS; PR00048; ZINCFINGER.

DR ProDom; PD000003; Znf_C2H2; 3.

DR SMART; SM00355; Znf_C2H2; 6.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.

KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;

KW Nuclear protein; Repeat.

FT NON_TER 1 1

FT ZN_FING <1 19 C2H2-TYPE.

FT ZN_FING 25 47 C2H2-TYPE.

FT ZN_FING 53 75 C2H2-TYPE.

FT ZN_FING 81 102 C2H2-TYPE (ATYPICAL).

FT ZN_FING 108 130 C2H2-TYPE.

FT ZN_FING 136 158 C2H2-TYPE.

FT ZN_FING 164 186 C2H2-TYPE.

FT ZN_FING 192 214 C2H2-TYPE.

FT ZN_FING 220 242 C2H2-TYPE (ATYPICAL).
SQ SEQUENCE 247 AA; 28448 MW; 5AB5B6F46C3234E2 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
|||||||
Db 20 TGEKPYK 26

RESULT 12

ZN80_GORGO

ID ZN80_GORGO STANDARD; PRT; 273 AA.

AC P51503;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Zinc finger protein 80.

GN ZNF80.

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9595;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96036504; PubMed=7483274;

RA di Cristofano A., Strazzullo M., Parisi T., la Mantia G.;

RT "Mobilization of an ERV9 human endogenous retroviral element during
RT primate evolution.";

RL Virology 213:271-275(1995).

CC -!- FUNCTION: May be involved in transcriptional regulation.

CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.

CC -!- SIMILARITY: Contains 7 C2H2-type zinc fingers.

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CC -----

DR EMBL; X89631; CAA61773.1; -.

DR InterPro; IPR007087; Znf_C2H2.

DR InterPro; IPR007086; Znf_C2H2_sub.

DR Pfam; PF00096; zf-C2H2; 7.

DR PRINTS; PR00048; ZINCFINGER.

DR ProDom; PD000003; Znf_C2H2; 5.

DR SMART; SM00355; ZnF_C2H2; 6.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.

KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;

KW Nuclear protein; Repeat.

```

FT  ZN_FING      49      71      C2H2-TYPE 1.
FT  ZN_FING      77      99      C2H2-TYPE 2.
FT  ZN_FING     105     127      C2H2-TYPE 3 (ATYPICAL).
FT  ZN_FING     133     155      C2H2-TYPE 4.
FT  ZN_FING     161     183      C2H2-TYPE 5.
FT  ZN_FING     189     211      C2H2-TYPE 6.
FT  ZN_FING     217     239      C2H2-TYPE 7.
SQ  SEQUENCE    273 AA;  31256 MW;  E9378A222898BDF1 CRC64;

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Query Match          100.0%;  Score 40;  DB 1;  Length 273;
Best Local Similarity 100.0%;  Pred. No. 0.45;
Matches      7;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          1 TGEKPYK 7
            |||||
Db          184 TGEKPYK 190

```

RESULT 13

Z253_HUMAN

ID Z253_HUMAN STANDARD; PRT; 275 AA.

AC O75346;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Zinc finger protein 253 (Bone marrow zinc finger 1) (BMZF-1).

GN ZNF253 OR BMZF1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=20054457; PubMed=10585455;

RA Han Z.-G., Zhang Q.-H., Ye M., Kan L.-X., Gu B.-W., He K.-L.,

RA Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., Chen Z.;

RT "Molecular cloning of six novel Kruppel-like zinc finger genes from

RT hematopoietic cells and identification of a novel transregulatory

RT domain KRNB.";

RL J. Biol. Chem. 274:35741-35748(1999).

CC -!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR. SEEM TO HAVE A
CC TRANSCRIPTIONAL REPRESSION ACTIVITY.

CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW AND IN MONOCYTIC AND
CC IMMATURE ERYTHROID CELL LINES.

CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.

CC -!- SIMILARITY: Contains 1 KRAB domain.

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CC -----
 DR EMBL; AF038951; AAC26844.1; -.
 DR HSSP; P08046; 1AII.
 DR Genew; HGNC:13497; ZNF253.
 DR MIM; 606954; -.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0016564; F:transcriptional repressor activity; NAS.
 DR GO; GO:0008270; F:zinc ion binding; NAS.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro; IPR001909; KRAB.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 3.
 DR SMART; SM00349; KRAB; 1.
 DR SMART; SM00355; ZnF_C2H2; 3.
 DR PROSITE; PS50805; KRAB; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat; Repressor.
 FT DOMAIN 4 75 KRAB.
 FT ZN_FING 172 194 C2H2-TYPE.
 FT ZN_FING 200 222 C2H2-TYPE.
 FT ZN_FING 228 250 C2H2-TYPE.
 SQ SEQUENCE 275 AA; 31929 MW; 8D6FE98439F487C2 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 275;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 223 TGEKPYK 229

RESULT 14

ZG46_XENLA
 ID ZG46_XENLA STANDARD; PRT; 280 AA.
 AC P18722;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Gastrula zinc finger protein XLCGF46.1 (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poeting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";

RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06572; S06572.
 DR HSSP; P08047; 1SP2.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 10.
 DR SMART; SM00355; ZnF_C2H2; 10.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 10.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.
 FT ZN_FING 146 168 C2H2-TYPE.
 FT ZN_FING 174 196 C2H2-TYPE.
 FT ZN_FING 202 224 C2H2-TYPE.
 FT ZN_FING 230 252 C2H2-TYPE.
 FT ZN_FING 258 280 C2H2-TYPE.
 FT NON_TER 280 280
 SQ SEQUENCE 280 AA; 32246 MW; F9CE819D49D49033 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
 |||||
 Db 253 TGEKPYK 259

RESULT 15

ZN75_HUMAN

ID ZN75_HUMAN STANDARD; PRT; 289 AA.
 AC P51815;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein 75.
 GN ZNF75.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung fibroblast;
 RX MEDLINE=94116987; PubMed=8288223;
 RA Villa A., Zucchi I., Pilia G., Strina D., Susani L., Morali F.,
 RA Patrosso C., Frattini A., Lucchini F., Repetto M., Sacco M.G.,
 RA Zoppe M., Vezzoni P.;
 RT "ZNF75: isolation of a cDNA clone of the KRAB zinc finger gene
 RT subfamily mapped in YACs 1 Mb telomeric of HPRT.";
 RL Genomics 18:223-229(1993).
 RN [2]
 RP SEQUENCE OF 139-289 FROM N.A.

RA Marino M., Archidiacono N., Franze N., Rosati M., Rocchi M.,
 RA Ballabio A., Grimaldi G.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: May be involved in transcriptional regulation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -!- SIMILARITY: Contains 1 KRAB domain.
 CC -!- SIMILARITY: Contains 5 C2H2-type zinc fingers.
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 CC -----
 DR EMBL; S67970; AAB29696.1; -.
 DR EMBL; X68010; CAA48147.1; -.
 DR PIR; A48913; A48913.
 DR HSSP; P25490; 1ZNM.
 DR Genew; HGNC:13145; ZNF75.
 DR MIM; 314997; -.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003677; F:DNA binding; NAS.
 DR GO; GO:0008270; F:zinc ion binding; NAS.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro; IPR001909; KRAB.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 3.
 DR SMART; SM00349; KRAB; 1.
 DR SMART; SM00355; ZnF_C2H2; 5.
 DR PROSITE; PS50805; KRAB; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 FT DOMAIN 14 97 KRAB.
 FT ZN_FING 144 166 C2H2-TYPE 1.
 FT ZN_FING 172 194 C2H2-TYPE 2.
 FT ZN_FING 200 222 C2H2-TYPE 3.
 FT ZN_FING 228 250 C2H2-TYPE 4.
 FT ZN_FING 256 278 C2H2-TYPE 5.
 SQ SEQUENCE 289 AA; 33683 MW; 96E7B00BF1DF64DE CRC64;

Query Match 100.0%; Score 40; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGEKPYK 7
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 Db 167 TGEKPYK 173

Search completed: March 5, 2004, 16:23:41
Job time : 1.95062 secs